



SEQUENCE LISTING

<110> Itadani, Hiraku
Takimura, Tetsuo
Nakamura, Takao
Kobayashi, Masahiko
Tanaka, Ken-ichi
Hidaka, Yusuke
Ohta, Masataka

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)
BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

<130> 06501-083001

<140> 09/891,053

<141> 2001-06-25

<150> PCT/JP99/07280

<151> 1999-12-24

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 11/145661

<151> 1999-05-25

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 413

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<213> Rattus norvegicus

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Trp	Thr	Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr
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65				70						75				80	
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Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val
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Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr					
	165		170		175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe					
	180		185		190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe					
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Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn					
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Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly					
225		230		235	240
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro					
	245		250		255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu					
	260		265		270
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu					
	275		280		285
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg					
	290		295		300
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg					
305		310		315	320
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly					
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Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys					
	340		345		350
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu					
	355		360		365
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His					
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Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu					
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<213> Rattus norvegicus

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gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc	96
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala	
20 25 30	
tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca	144
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr	
35 40 45	

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgg agc Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser 50 55 60	192
ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp 65 70 75 80	240
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gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile 115 120 125	384
agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala 130 135 140	432
cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp 145 150 155 160	480
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atc cag agg cgc acc cgc ctt cgg ctt gat ggg gcc cgt gag gct ggc Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly 225 230 235 240	720
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro 245 250 255	768
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cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 864
 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
 275 280 285

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 912
 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
 290 295 300

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tgg cgg 960
 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
 305 310 315 320

gac aag aag gtg gcc aag tgg ctg gcc atc atc gtg agc atc ttt ggg 1008
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
 325 330 335

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1056
 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
 340 345 350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1104
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
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ctg tgg gcc aac tgg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152
 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
 370 375 380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200
 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
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<212> DNA

<213> Rattus norvegicus

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tccgcccgtg	ccctgcccgg	tgtccccgag	ccgtgtgagc	ctgctggggc	atg gag	356
				Met Glu		
				1		

cgc	gcg	ccg	ccc	gac	ggg	ctg	atg	aac	gcg	tcg	ggc	act	ctg	gcc	gga	404
Arg	Ala	Pro	Pro	Asp	Gly	Leu	Met	Asn	Ala	Ser	Gly	Thr	Leu	Ala	Gly	
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Glu	Ala	Ala	Ala	Ala	Gly	Gly	Ala	Arg	Gly	Phe	Ser	Ala	Ala	Trp	Thr	
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gct	gtc	ctg	gct	gcg	ctc	atg	gcg	ctg	ctc	atc	gtg	gcc	aca	gta	ctg	500
Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr	Val	Leu	
	35				40					45				50		

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Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser	Leu	Arg	
		55					60						65			

acc	cag	aac	aac	ttc	ttt	ctg	ctc	aac	ctc	gcc	atc	tcc	gac	ttc	ctc	596
Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Phe	Leu	
		70					75					80				

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Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu	Thr	Gly	
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gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln 135 140 145	788
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Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys
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 Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Lys His Gly
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 cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg att ctg tgg 1450
 Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp
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 Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val
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 Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
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<211> 32

<212> DNA

<213> Artificial Sequence

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<223> artificially synthesized primer sequence

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32

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<212> DNA

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<212> DNA

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<211> 20

<212> DNA

<213> Artificial Sequence

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20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

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<221> exon

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<221> misc_feature

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60

120


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<210> 12
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> exon
 <222> (259) ... (425)

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gccgctggac cttcggccgg ggctctgca agctgtggct ggtagtggac tacctgctgt 360
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cgagcccccct	cccagggccc	agccctcacc	accccccacc	ctcggctgct	ggggctgctg	660
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aggcctctgag	gcccggggagg	cgacccctcg	gggtgggggt	gggggggggt	cctggtcttc	780
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cgccctgccc	ggccactgct	tccctgacta	ctggtaaggaa	acccctctct	ggctcctgtg	1080
ggccaaactcg	gctgtcaacc	ctgtcctcta	ccctctgtgc	caaccacagct	tcgcgcgggc	1140
cttcaccaag	ctgctctgcc	cccagaagct	caaaatccag	ccccacagct	ccctggagca	1200
ctgctggaag	tgagtggccc	accagagcct	ccctcagcga	cgccctctct	agcccaggtc	1260
tcctgggcat	ctggccctgc	tgcccccctac	ccggctcgtt	cccccagggg	tgagccccgc	1320
cgtgtctgtg	gccctctctt	aatgccacgg	cagccacccct	gcacatggagg	cgccttctctg	1380
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acattctggc	tccaccggga	gggacagtct	ggaggtccca	gacatgctgc	ccaccccctg	1500
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gggtgttttc	agaaagatga	agaagaaaac	atgtctgtga	acttgatgtt	cctgggatgt	1860
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<213> Artificial Sequence

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<210> 15

<211> 21

<212> DNA

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<223> artificially synthesized primer sequence

<400> 15

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<212> PRT
<213> Homo sapiens

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Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
35 40 45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
50 55 60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
85 90 95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
100 105 110
Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115	120	125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala		
130	135	140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp		
145	150	155
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr		
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Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe		
180	185	190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe		
195	200	205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn		
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Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala		
225	230	235
Gly Pro Glu Pro Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro Pro		
245	250	255
Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu		
260	265	270
His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu		
275	280	285
Ala Thr Leu Gly Gly Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr		
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Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu		
305	310	315
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg		
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Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg		
340	345	350
Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly		
355	360	365
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys		
370	375	380
His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu		
385	390	395
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His		
405	410	415
His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu		
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Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys		
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<211> 2050

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271)...(1629)

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aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctccg tcgcggagtc	180

gctgagtcog tgccttttta gttagttctg cagtctagta tggtecccat ttgccttcc	240
actcccgag cgcgctgagc ctgcgggggc atg gag cgc gcg ccg ccc gac ggg	294
Met Glu Arg Ala Pro Pro Asp Gly	
1 5	
ccg ctg aac gct teg ggg gcg ctg gcg ggc gag gcg gcg gcg gcg ggc	342
Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly	
10 15 20	
ggg gcg cgc ggc ttc teg gca gcc tgg acc gcg gtg ctg gcc gcg ctc	390
Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu	
25 30 35 40	
atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg	438
Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met	
45 50 55	
ctc gcc ttc gtg gcc gac teg agc ctc cgc acc cag aac aac ttc ttc	486
Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe	
60 65 70	
ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc	534
Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile	
75 80 85	
cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgg	582
Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg	
90 95 100	
ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc	630
Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser	
105 110 115 120	
tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg teg gtc	678
Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val	
125 130 135	
acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca	726
Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala	
140 145 150	
gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga	774
Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly	
155 160 165	
cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc	822
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro	
170 175 180	
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc	870
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile	
185 190 195 200	
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc	918
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe	
205 210 215	

ttt aac ctc agc atc tac ctg aac atc bag agg cgc acc cgc ctc cgg	956
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg	
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Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala	
235 240 245	
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag	1052
Gln Pro Ser Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys	
250 255 260	
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Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala	
265 270 275 280	
gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg	1158
Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly Gly	
285 290 295	
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Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg	
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ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg	1254
Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala	
315 320 325	
tcc tcg gcc tcg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc	1302
Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe	
330 335 340	
acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg	1350
Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu	
345 350 355 360	
gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg	1398
Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu	
365 370 375	
ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac	1446
Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr	
380 385 390	
tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac	1494
Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn	
395 400 405	
cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc	1542
Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr	
410 415 420	
aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg	1590
Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu	
425 430 435 440	
gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat	1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu
 445 450

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gcttctgccc accccgcctc tgggctcaca ccagccctgg tggccaagcc tgccccggcc 1819
actctgtttg ctcacccagg acctctgggg gttgttggga ggagggggcc cggttgggccc 1879
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ccatgtgctg tgcacccgtg ccacgcgctc tgcattgctc tatgctgtg ccgctgcgc 1999
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<211> 20

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<213> Artificial Sequence

<220>

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<221> misc_feature

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<400> 22

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<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 23

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<400> 24

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<210> 25

<211> 445

<212> PRT

<213> Rattus norvegicus

<400> 25

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Trp	Thr	Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr
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Leu	Arg	Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp
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Phe	Leu	Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu
				85					90					95	
Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val
			100					105					110		
Val	Asp	Tyr	Leu	Leu	Cys	Ala	Ser	Ser	Val	Phe	Asn	Ile	Val	Leu	Ile
	115						120					125			
Ser	Tyr	Asp	Arg	Phe	Leu	Ser	Val	Thr	Arg	Ala	Val	Ser	Tyr	Arg	Ala
	130					135					140				
Gln	Gln	Gly	Asp	Thr	Arg	Arg	Ala	Val	Arg	Lys	Met	Ala	Leu	Val	Trp
145					150					155					160
Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr
			165					170					175		
Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe
		180						185					190		
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe
	195						200					205			
Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn
	210					215					220				
Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly
225					230					235					240
Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro
				245					250					255	
Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu
		260						265					270		
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu
	275						280					285			
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	290					295					300				
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu
305					310				315						320
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg
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Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg
		340						345					350		
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly
	355						360					365			
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys
	370					375					380				
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu
385					390					395					400
Leu	Trp	Ala	Asn	Ser	Ala	Val	Asn	Pro	Val	Leu	Tyr	Pro	Leu	Cys	His
			405						410					415	
Tyr	Ser	Phe	Arg	Arg	Ala	Phe	Thr	Lys	Leu	Leu	Cys	Pro	Gln	Lys	Leu
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 <212> DNA
 <213> Rattus norvegicus

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 <222> (302)...(1636)

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 aaaaccgggc tgggcgaaga gccggcaaag attaggtca cgagcggggg ccccaaccgg 240
 ccaccagct ctccgccgt gccctgcccg gtgtcccca gccgtgtgag cctgtgggc 300
 c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 349
 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1 5 10 15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 397
 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 445
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc 493
 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 541
 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 589
 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg 637
 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 100 105 110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc 685
 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
 115 120 125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 733
 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
 130 135 140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 781
 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
 145 150 155 160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 829

Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr		
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Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe		
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ttc	tac	aac	tgg	tac	ttt	ctc	atc	acg	gcc	tcc	acc	ctc	gag	ttc	ttc	925	
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe		
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Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn		
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Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly		
225				230				235					240				
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Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro		
			245					250					255				
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Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu		
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cac	agg	tat	ggg	gtg	ggg	gag	gca	ggc	cct	ggg	gtt	gag	gct	ggg	gag	1165	
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu		
		275				280					285						
gct	gcc	ctc	ggg	ggg	ggc	agt	ggg	gga	ggg	gct	gct	gcc	tgc	ccc	acc	1213	
Ala	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ala	Ala	Ala	Ser	Pro	Thr		
	290					295				300							
tcc	agc	tct	ggc	agc	tcc	tca	agg	ggc	act	gag	agg	cca	cgc	tca	ctc	1261	
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu		
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Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg		
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atg	aag	atg	gtg	tcc	cag	agc	atc	acc	cag	cgc	ttc	cgg	ctg	tgc	cgg	1357	
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg		
		340					345					350					
gac	aag	aag	gtg	gcc	aag	tgc	ctg	gcc	atc	atc	gtg	agc	atc	ttt	ggg	1405	
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly		
		355				360					365						
ctc	tgc	tgg	gcg	ccg	tac	acg	ctc	cta	atg	atc	atc	cga	gct	gct	tgc	1453	
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys		
	370					375					380						
cat	ggc	cgc	tgc	atc	ccc	gat	tac	tgg	tac	gag	acg	tcc	ttc	tgg	ctt	1501	
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu		

335	390	395	400	
ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac				1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His				
	405	410	415	
tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc				1597
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu				
	420	425	430	
aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg				1646
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys				
	435	440	445	
ccccaccctt ctgaggccag gcccttgtae ttgtttgagt gggcagccgg agcgtgggag				1706
gggccctggt ccatgctccg ctccaaatgc catgggggag tottagatca tcaaccccgc				1766
agtggggtag catggcaggt gggccaagag cctagttgg tggagctaga gtgtgctggt				1826
tagctctgcc gcacattctc cttcaccaca cagaagagac aatccaggag tcccaggcat				1886
gccttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag				1946
tgatgtc				1953